

2590
2530#3
OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/010,720

DATE: 05/31/2002
 TIME: 11:58:05

Input Set : A:\LEX-0382-USA SEQLIST.txt
 Output Set: N:\CRF3\05312002\J010720.raw

4 <110> APPLICANT: Walke, D. Wade
 5 Hilbun, Erin
 6 Donoho, Gregory
 7 Turner, C. Alexander Jr.
 8 Hansen, Gwenn
 9 BeltranelRio, Hector
 10 Van Sligtenhorst, Isaac
 12 <120> TITLE OF INVENTION: Novel Human Kinases and Polynucleotides
 Encoding the Same, And Uses Thereof
 13
 15 <130> FILE REFERENCE: LEX-0382-USA
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/010,720
 C--> 17 <141> CURRENT FILING DATE: 2002-05-21
 17 <150> PRIOR APPLICATION NUMBER: US 60/206,015
 18 <151> PRIOR FILING DATE: 2000-05-19
 20 <150> PRIOR APPLICATION NUMBER: US 09/854,856
 21 <151> PRIOR FILING DATE: 2000-05-14
 23 <160> NUMBER OF SEQ ID NOS: 64
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 7149
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <400> SEQUENCE: 1

| | | | | | | |
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| 34 ccggctcctg | ccccaaagaa | tggctccagc | tccgattcct | ccgtggggga | gaaactggga | 120 |
| 35 gcccggccg | ccgacgtgt | gaccggcagg | accgaggagt | acaggcgccg | ccgccccact | 180 |
| 36 atggacaagg | acagccgtgg | ggcggccgcg | accactacca | ccactgagca | ccgcttcttc | 240 |
| 37 cgccggagcg | tcatctgcga | ctccaatgcc | actgcactgg | agcttcccg | ccttccttct | 300 |
| 38 tccctgcccc | agcccagcat | ccccggcgct | gtcccgcaga | gtgctccacc | ggagccccac | 360 |
| 39 cggaaagaga | ccgtgaccgc | caccggccact | tcccaggtag | cccagcagcc | tccagccgt | 420 |
| 40 gccggccctg | gggaacaggc | cgtcggggc | cctgccccct | cgactgtccc | cagcagtacc | 480 |
| 41 agcaaagacc | gcccagtgtc | ccagccttagc | cttgtggga | gcaaagagga | gccggcccg | 540 |
| 42 gcgagaagt | gcagcggcgg | cgccagcgcc | aaggagccac | aggaggaacg | gagccagcag | 600 |
| 43 caggatata | tcgaagagct | ggagaccaag | gccgtggaa | tgtctaacga | tggccgttt | 660 |
| 44 ctaaagttt | acatcgaaat | cgccagaggc | tcctttaaga | cggtctacaa | aggcttgac | 720 |
| 45 actgaaaacca | ccgtgaaat | cgccctgggt | gaactgcagg | atcgaaaatt | aacaaagtct | 780 |
| 46 gagaggcaga | gatttaaaga | agaagctgaa | atgttaaaag | gtcttcagca | tcccaatatt | 840 |
| 47 gttagattt | atgattcctg | ggaatccaca | gtaaaaggaa | agaagtgcatt | tgtttggtg | 900 |
| 48 actgaactta | tgacgtctgg | aacacttaaa | acgtatctga | aaaggtttaa | agtgtatgaag | 960 |
| 49 atcaaagttc | taagaagctg | gtgccgtcag | atccttaaag | gtcttcagtt | tcttcatact | 1020 |
| 50 cgaactccac | ctatcattca | ccgcgatctt | aaatgtgaca | acatctttat | cacccggccct | 1080 |
| 51 actggctcag | tcaagattgg | agacctcggt | ctggcaaccc | tgaagcgggc | ttctttgcc | 1140 |
| 52 aagagtgtga | tagtacccc | agagttcatg | gcccctgaga | tgtatgagga | gaaatatgat | 1200 |

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|-----|--|------|
| 53 | gaatccgttg acgttatgc tttggatg tgcatgctt agatggctac atctaatat | 1260 |
| 54 | ccttaactcg agtccaaaaa tgctgcacag atctaccgtc gcgtgaccag tgggtgaaag | 1320 |
| 55 | ccagccagtt ttgacaaaagt agcaattcct gaagtgaagg aaattattga aggatgcata | 1380 |
| 56 | cgacaaaaca aagatgaaag atattccatc aaagaccttt tgaaccatgc cttttccaa | 1440 |
| 57 | gagggaaacag gagtacgggt agaatttagca gaagaagatg atggagaaaa aatagccata | 1500 |
| 58 | aaattatggc tacgtattga agatattaag aaattaaagg gaaaatacaa agataatgaa | 1560 |
| 59 | gctattttagt ttttttga ttttagagaga gatgtcccag aagatgttc acaagaaatg | 1620 |
| 60 | gttagtctg ggtatgtctg tgaaggtgat cacaagacca tggctaaagc tatcaaagac | 1680 |
| 61 | agagtatcat taattaagag gaaacgagag cagcggcagt tggtaacggg ggagcaagaa | 1740 |
| 62 | aaaaaaaaago aggaagagag cagtctcaaa cagcaggtag aacaatccag tgcttcccag | 1800 |
| 63 | acaggaatca agcagctccc ttctgcttagc accggcatac ctactgcttc taccacttca | 1860 |
| 64 | gcttcagttt ctacacaagt agaacctgaa gaacctgagg cagatcaaca tcaacaacta | 1920 |
| 65 | cagtaaccgc aacccagtt atctgtgtta tctgtatggg cgggtgacag tggtcaggga | 1980 |
| 66 | tcctctgtct tcacagaatc tcgagtggc agccaacaga cagtttcata tggttccaa | 2040 |
| 67 | catgaacagg cacattctac aggcacagtc ccagggcata taccttctac tgtccaagca | 2100 |
| 68 | cagtctcagc cccatgggt atatccaccc tcaagtgtgg cacagggca gagccagggt | 2160 |
| 69 | cagccatcct caagtagctt aacaggggtt tcatcttccc aaccatatac acatcctcag | 2220 |
| 70 | cagcagcagg gaatacagca gacagccccct cctcaacaga cagtgcagta ttcaacttca | 2280 |
| 71 | cagacatcaa cctccagtga gcccactact gcacagccag tgagtccagcc tcaagctcca | 2340 |
| 72 | caagtcttgc ctcaagtttc agctggaaaaa cagcttccag tttcccagcc agtaccaact | 2400 |
| 73 | atccaaggcg aacctcagat cccagttcg acacaaccct cgggtgttcc agtccactct | 2460 |
| 74 | ggtgcttattt tccttcagg gggacagccg ctccctactc cttgtctccc tcagttaccct | 2520 |
| 75 | gtctctcaga ttcccatatc aactcctcat gtgtctacgg ctcagacagg tttctcatcc | 2580 |
| 76 | cttcccatca caatggcagc tggcattact cagcctctgc tcacgttggc ttcatctgct | 2640 |
| 77 | acaacagctg cgatccggg ggtatcaact gtggttccca gtcagttcc aacccttctg | 2700 |
| 78 | cagccgttga ctcaagtc aagtcaaggta caccacagc tcctacaacc agcagttcag | 2760 |
| 79 | tccatggaa taccagctaa cttggacaa gctgctgagg ttccacttcc ctctggagat | 2820 |
| 80 | gttctgtacc agggctccc acctcgactg ccaccacagt acccaggaga ttcaaatatt | 2880 |
| 81 | gctcccttcc ccaacgttgc ttctgtttgc atccattcta cagtcctawc ccctccatg | 2940 |
| 82 | ccgacagaag tactggctac acctgggtac tttccacag tggtgccagcc ttatgtggaa | 3000 |
| 83 | tcaaatctt tagttctat ggggtgtta ggaggacagg ttcagtgcc ccagccagga | 3060 |
| 84 | gggagtttag cacaagcccc cactacatcc tcccagcaag cagttttggg ggtactcag | 3120 |
| 85 | ggagtctctc aggttgc tgcagagccca gttcagtag cacaagcccc agctacccag | 3180 |
| 86 | ccgaccactt tggcttccctc ttagacagt gcacattcag atgttgc ttc aggtatgagt | 3240 |
| 87 | gatggcaatg agaacgtccc atctccatg ggaaggcatg aaggaagaac tacaaaacgg | 3300 |
| 88 | cattaccgaa aatctgttaag gatgcgttgc cagatgaaa aaacttcacg cccaaaatta | 3360 |
| 89 | agaattttga atgttcaaa taaggagac cgatgttgc aatgtcaatt agagactcat | 3420 |
| 90 | aataggaaaa tggttacatt caaatttgac ctatgtgtt gcaaccccgaa ggagatagca | 3480 |
| 91 | acaattatgg tgaacaatga ctttattcta gcaatagaga gagatgttgc tttatgttgc | 3540 |
| 92 | gtgcgagaaa ttattgaaaa agctgtatgaa atgtcgttgc aggtatgttgc tttatgttgc | 3600 |
| 93 | gaggggtatc agggatggaa ggttccatca ggttccatca ggttccatca ggttccatca | 3660 |
| 94 | cagaaatgg aaggagatg caaacaacca attcctgcgt cttccatgcc acagcaata | 3720 |
| 95 | ggcatttccca ccagttccca aactcaagtt gttcattctg cgggaaggcc gtttatagttgc | 3780 |
| 96 | agtccgttgc cagaaagccg attacgagaa tcaaaatgtt tcccttgc aataacagat | 3840 |
| 97 | acagttgttgc cctctacatc tcagagccct ggttccatca ggttccatca ggttccatca | 3900 |
| 98 | cttagtctac aacaggccctt ttctgttgc tttatgttgc gtttatagttgc tttatgttgc | 3960 |
| 99 | acagcaccc tcatacagga ccaacatttc cagtagtacc tcctttctt aataacagat | 4020 |
| 100 | atgttccatca tttatgttgc gtttatagttgc tttatgttgc gtttatagttgc tttatgttgc | 4080 |
| 101 | agcccttccca atgttccatca tttatgttgc gtttatagttgc tttatgttgc tttatgttgc | 4140 |

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|-----|-------------|-------------|-------------|--------------|--------------|--------------|------|
| 102 | gaggggattt | ctggagttgc | caccagcaca | ggtgtggtaa | cttcaggtgg | tctccata | 4200 |
| 103 | ccacactgtgt | ctgaatcacc | agtactttcc | agcgtagttt | caagtatcac | aatacctgca | 4260 |
| 104 | gttgtctcaa | tatctactac | atccccgtca | cttcaagtcc | ccacatccac | atctgagatc | 4320 |
| 105 | gttgtttcta | gtacagcaact | gtatccttca | gtaacagttt | cagcaacttc | agcctctgca | 4380 |
| 106 | gggggcagta | ctgctacccc | aggtcctaag | cctccagctg | tagtatctca | gcaggcagca | 4440 |
| 107 | ggcagcaacta | ctgtgggagc | cacattaaca | tcagtttcta | ccaccacttc | attccaagc | 4500 |
| 108 | acagcttcac | agctgtccat | tcagotttgc | agcagtaactt | ctactcctac | tttagctgaa | 4560 |
| 109 | accgtggtag | ttagcgcaca | ctcaactagat | aagacatctc | atagcagttac | aactggattt | 4620 |
| 110 | gttttctccc | tctctgcacc | atcttcctct | tcctctctg | gagcaggagt | gtctagttat | 4680 |
| 111 | atttctcagc | ctggggggt | gcatttttg | gtcattccat | cagtatagtc | ttctactcct | 4740 |
| 112 | attcttcccc | aagcagcagg | acctacttct | acacccctt | taccccaagt | accttagtac | 4800 |
| 113 | ccacccttgg | tacaggctgt | tgccaatgtg | cctgctgtac | agcagacact | aattcatagt | 4860 |
| 114 | cagcctcaac | cagcttgc | tcccaaccag | ccccatactc | attgtcctga | agtagattct | 4920 |
| 115 | gatacacaac | ccaaagctcc | tggaatttgc | gacataaaga | ctctagaaga | aaagctgcgg | 4980 |
| 116 | tctctgttca | gtgaacacag | ctcatcttgc | gctcagcatg | cctctgtctc | actggagacc | 5040 |
| 117 | tcacttagtca | tagagagcac | tgtcacacca | ggcatccaa | ctactgtgt | tgcaccaage | 5100 |
| 118 | aaactcctga | cttctaccac | aagtacttgc | ttaccacca | ccaatttacc | actaggaaca | 5160 |
| 119 | gtgctttgc | cagttacacc | agtggtcaca | cctggcaag | tttctacccc | agtcagcaact | 5220 |
| 120 | actacatca | gagtggaaacc | ttgaactgt | cccttcaagc | cacctctaac | taaggctccg | 5280 |
| 121 | gtgctgccag | tgggtactga | acttccagca | ggtaactctac | ccagcggca | gctgccacct | 5340 |
| 122 | tttccaggac | cttctctaac | ccagttccag | caacctctac | aggatcttgc | tgctcaatttgc | 5400 |
| 123 | agaagaacac | ttagttccaga | gatkatcaca | gtgacttctg | cggttggtcc | tgtgtccatg | 5460 |
| 124 | gcccgtccaa | cagcaatcac | agaaggcagg | acacagctc | agaagggtgt | ttctcaagtc | 5520 |
| 125 | aaagaaggcc | ctgtccttagc | aacttagttc | ggagctggtg | tttttaagat | gggacgattt | 5580 |
| 126 | cagggttctg | ttgcagcaga | cggtgcccag | aaagagggtt | aaaataagtc | agaagatgca | 5640 |
| 127 | aagtctgttc | attttgaatc | cagcacctca | gagtcctcag | tgctatcaag | tagtagtcca | 5700 |
| 128 | gagagtacct | tggtaaaacc | agagccgaat | ggcataacca | tccctggat | ctcttcagat | 5760 |
| 129 | gtgccagaga | gtgcccacaa | aactactgccc | tcagaggca | agtcagacac | tggcagcct | 5820 |
| 130 | accaagggtt | gacgtttca | gtgtacaact | acagcaaaca | aagtgggtcg | tttctctgttca | 5880 |
| 131 | tcaaaaaactg | aggacaagat | cactgacaca | aagaaagaag | gaccagtggc | atctccctct | 5940 |
| 132 | tttatggatt | tggaaacaagc | tgttcttct | gctgtatac | caaagaaaga | gaagcctgaa | 6000 |
| 133 | ctgtcagac | cttcacatct | aaatggccg | tcttctgacc | cgaggccgc | tttttaagt | 6060 |
| 134 | aggatgtgg | atgatggttc | cggtagtcca | cactcgcccc | atcagctgag | ctcaaagagc | 6120 |
| 135 | cttcctagcc | agaatctaag | tcaaagcctt | agtaattcat | ttaactcctc | ttacatgagt | 6180 |
| 136 | agcgacaatg | agtcaagat | cgaagatgaa | gactaaagt | tagactgctg | acgactacga | 6240 |
| 137 | gataaacatc | tcaaagagat | tcaggacctt | cagactcgcc | agaagcatga | aattgaatct | 6300 |
| 138 | ttgtataccca | aactggca | ggtgcacccct | gctgttatta | ttccccccagc | tgctccctt | 6360 |
| 139 | tcagggagaa | gacgacgacc | cactaaaagc | aaaggcagca | aatcttagtgc | aaggcgttcc | 6420 |
| 140 | ttggggaaata | aaagccccca | gttttcagg | aacctgtctg | gtcagagtgc | agcttcagtc | 6480 |
| 141 | ttgcacccccc | agcagaccct | ccacccttct | ggcaacatcc | cagagtccgg | gcagaatcag | 6540 |
| 142 | ctgttacagc | cccttaagcc | atctccctcc | agtgacaacc | tctattcagc | tttcaccagt | 6600 |
| 143 | gatggtgcca | tttcagttacc | aagcctttct | gctccaggc | aaggaaccag | cagcacaaac | 6660 |
| 144 | actgttgggg | caacagtgaa | cagccaagcc | gcccaagctc | agcctcctgc | catgacgtcc | 6720 |
| 145 | agcaggaagg | gcacattcac | agatgacttgc | cacaagttgg | tagacaatttgc | ggcccggat | 6780 |
| 146 | gcatgaatc | tctcaggcag | gagaggaagc | aaagggcaca | tgaattatgc | ggccctggaa | 6840 |
| 147 | atggcaagga | agttctctgc | acctgggca | ctgtcatct | ccatgacccct | gaacctgggt | 6900 |
| 148 | ggctctgccc | ccatctctgc | agcatcagct | acctctctag | gtcacttcac | caagtctatg | 6960 |
| 149 | tgcacccac | agcagtttgc | tttccacatgt | acccatatttgc | gctcaatgc | gatggggacg | 7020 |
| 150 | gttggccag | caccacagcc | acttggccag | ttccaacctg | tggaaactgc | ctccttgcag | 7080 |

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151 aatttcaaca tcagcaattt gcagaaatcc atcagcaacc ccccaggctc caacctgcgg    7140
152 accacttag                                         7149
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 2382
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapiens
161 <220> FEATURE:
162 <221> NAME/KEY: VARIANT
163 <222> LOCATION: (1)...(2382)
164 <223> OTHER INFORMATION: Xaa = Any Amino Acid
166 <400> SEQUENCE: 2
167 Met Ser Gly Gly Ala Ala Glu Lys Gln Ser Ser Thr Pro Gly Ser Leu
168   1           5           10          15
169 Phe Leu Ser Pro Pro Ala Pro Ala Pro Lys Asn Gly Ser Ser Ser Asp
170   20          25          30
171 Ser Ser Val Gly Glu Lys Leu Gly Ala Ala Ala Ala Asp Ala Val Thr
172   35          40          45
173 Gly Arg Thr Glu Glu Tyr Arg Arg Arg Arg His Thr Met Asp Lys Asp
174   50          55          60
175 Ser Arg Gly Ala Ala Ala Thr Thr Thr Thr Glu His Arg Phe Phe
176   65          70          75          80
177 Arg Arg Ser Val Ile Cys Asp Ser Asn Ala Thr Ala Leu Glu Leu Pro
178   85          90          95
179 Gly Leu Pro Leu Ser Leu Pro Gln Pro Ser Ile Pro Ala Ala Val Pro
180   100         105         110
181 Gln Ser Ala Pro Pro Glu Pro His Arg Glu Glu Thr Val Thr Ala Thr
182   115         120         125
183 Ala Thr Ser Gln Val Ala Gln Gln Pro Pro Ala Ala Ala Pro Gly
184   130         135         140
185 Glu Gln Ala Val Ala Gly Pro Ala Pro Ser Thr Val Pro Ser Ser Thr
186   145         150         155         160
187 Ser Lys Asp Arg Pro Val Ser Gln Pro Ser Leu Val Gly Ser Lys Glu
188   165         170         175
189 Glu Pro Pro Ala Arg Ser Gly Ser Gly Gly Ser Ala Lys Glu
190   180         185         190
191 Pro Gln Glu Glu Arg Ser Gln Gln Asp Asp Ile Glu Glu Leu Glu
192   195         200         205
193 Thr Lys Ala Val Gly Met Ser Asn Asp Gly Arg Phe Leu Lys Phe Asp
194   210         215         220
195 Ile Glu Ile Gly Arg Gly Ser Phe Lys Thr Val Tyr Lys Gly Leu Asp
196   225         230         235         240
197 Thr Glu Thr Thr Val Glu Val Ala Trp Cys Glu Leu Gln Asp Arg Lys
198   245         250         255
199 Leu Thr Lys Ser Glu Arg Gln Arg Phe Lys Glu Glu Ala Glu Met Leu
200   260         265         270
201 Lys Gly Leu Gln His Pro Asn Ile Val Arg Phe Tyr Asp Ser Trp Glu
202   275         280         285
203 Ser Thr Val Lys Gly Lys Lys Cys Ile Val Leu Val Thr Glu Leu Met
204   290         295         300

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205 Thr Ser Gly Thr Leu Lys Thr Tyr Leu Lys Arg Phe Lys Val Met Lys
 206 305 310 315 320
 207 Ile Lys Val Leu Arg Ser Trp Cys Arg Gln Ile Leu Lys Gly Leu Gln
 208 325 330 335
 209 Phe Leu His Thr Arg Thr Pro Pro Ile Ile His Arg Asp Leu Lys Cys
 210 340 345 350
 211 Asp Asn Ile Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Ile Gly Asp
 212 355 360 365
 213 Leu Gly Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile
 214 370 375 380
 215 Gly Thr Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp
 216 385 390 395 400
 217 Glu Ser Val Asp Val Tyr Ala Phe Gly Met Cys Met Leu Glu Met Ala
 218 405 410 415
 219 Thr Ser Glu Tyr Pro Tyr Ser Glu Cys Gln Asn Ala Ala Gln Ile Tyr
 220 420 425 430
 221 Arg Arg Val Thr Ser Gly Val Lys Pro Ala Ser Phe Asp Lys Val Ala
 222 435 440 445
 223 Ile Pro Glu Val Lys Glu Ile Ile Glu Gly Cys Ile Arg Gln Asn Lys
 224 450 455 460
 225 Asp Glu Arg Tyr Ser Ile Lys Asp Leu Leu Asn His Ala Phe Phe Gln
 226 465 470 475 480
 227 Glu Glu Thr Gly Val Arg Val Glu Leu Ala Glu Glu Asp Asp Gly Glu
 228 485 490 495
 229 Lys Ile Ala Ile Lys Leu Trp Leu Arg Ile Glu Asp Ile Lys Lys Leu
 230 500 505 510
 231 Lys Gly Lys Tyr Lys Asp Asn Glu Ala Ile Glu Phe Ser Phe Asp Leu
 232 515 520 525
 233 Glu Arg Asp Val Pro Glu Asp Val Ala Gln Glu Met Val Glu Ser Gly
 234 530 535 540
 235 Tyr Val Cys Glu Gly Asp His Lys Thr Met Ala Lys Ala Ile Lys Asp
 236 545 550 555 560
 237 Arg Val Ser Leu Ile Lys Arg Lys Arg Glu Gln Arg Gln Leu Val Arg
 238 565 570 575
 239 Glu Glu Gln Glu Lys Lys Gln Glu Glu Ser Ser Leu Lys Gln Gln
 240 580 585 590
 241 Val Glu Gln Ser Ser Ala Ser Gln Thr Gly Ile Lys Gln Leu Pro Ser
 242 595 600 605
 243 Ala Ser Thr Gly Ile Pro Thr Ala Ser Thr Thr Ser Ala Ser Val Ser
 244 610 615 620
 245 Thr Gln Val Glu Pro Glu Glu Pro Glu Ala Asp Gln His Gln Gln Leu
 246 625 630 635 640
 247 Gln Tyr Gln Gln Pro Ser Ile Ser Val Leu Ser Asp Gly Thr Val Asp
 248 645 650 655
 249 Ser Gly Gln Gly Ser Ser Val Phe Thr Glu Ser Arg Val Ser Ser Gln
 250 660 665 670
 251 Gln Thr Val Ser Tyr Gly Ser Gln His Glu Gln Ala His Ser Thr Gly
 252 675 680 685
 253 Thr Val Pro Gly His Ile Pro Ser Thr Val Gln Ala Gln Ser Gln Pro

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/010,720

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Input Set : A:\LEX-0382-USA SEQLIST.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 977,1808
Seq#:4; Xaa Pos. 977,1808
Seq#:6; Xaa Pos. 977
Seq#:8; Xaa Pos. 824,1655
Seq#:10; Xaa Pos. 824,1655
Seq#:12; Xaa Pos. 824
Seq#:14; Xaa Pos. 1562
Seq#:16; Xaa Pos. 1562
Seq#:18; Xaa Pos. 949,1780
Seq#:20; Xaa Pos. 949,1780
Seq#:22; Xaa Pos. 949
Seq#:24; Xaa Pos. 796,1627
Seq#:26; Xaa Pos. 796,1627
Seq#:28; Xaa Pos. 796
Seq#:30; Xaa Pos. 1534
Seq#:32; Xaa Pos. 1534
Seq#:34; Xaa Pos. 917,1748
Seq#:36; Xaa Pos. 917,1748
Seq#:38; Xaa Pos. 917
Seq#:40; Xaa Pos. 764,1595
Seq#:42; Xaa Pos. 764,1595
Seq#:44; Xaa Pos. 764
Seq#:46; Xaa Pos. 1502
Seq#:48; Xaa Pos. 1502
Seq#:50; Xaa Pos. 889,1720
Seq#:52; Xaa Pos. 889,1720
Seq#:54; Xaa Pos. 889
Seq#:56; Xaa Pos. 736,1567
Seq#:58; Xaa Pos. 736,1567
Seq#:60; Xaa Pos. 736
Seq#:62; Xaa Pos. 1474
Seq#:64; Xaa Pos. 1474